SEQUENCE LISTING

<110> Jialin, Sun

<120> A superantigen fusion protein for anti-cancer therapy and methods for the production thereof

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<141> 2006-03-15

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<151> 2004-05-31

<150> CN 200310109829.7
<151> 2003-12-21

<160> 15

<170> PatentIn version 3.1

<210> 1
<211> 903
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(903)
<223> coding sequence of fusion protein

<400> 1
aattccgata gcgagtgtcc tctgagtcac gatggttact gtctacatga cggcgtctgt 60
atgtatattg aggctctaga caagtacgcg tgtaattgcg ttgttggcta catcggtgag 120
cgctgtcagt atcgagatct gaaatggtgg gaacttagag gtggaggcgg ttcaggcgga 180
ggtggctctg gcggtggcgg atcgagcgag aaaagcgaag aaataaatga aaaagatttg 240
cgaaaaaagt ctgaattgca gggaacagct ttaggcaatc ttaaacaaat ctattattac 300
aatgaaaaag ctaaaactga aaataaagag agtcacgatc aatttttaca gcatactata 360
ttgtttaaag gctttttttac agatcattcg tggtataacg atttattagt agattttgat 420
tcaaaggata ttgttgataa atataaaggg aaaaaagtag acttgtatgg tgcttattat 480
ggttatcaat gtgcgggtgg tacaccaaac aaaacagctt gtatgtatgg tggtgtaacg 540
ttacatgata ataatcgatt gaccgaagag aaaaaagtgc cgatcaattt atggctagac 600
ggtaaacaaa atacagtacc tttggaaacg gttaaaacga ataagaaaaa tgtaactgtt 660
caggagttgg atcttcaagc aagacgttat ttacaggaaa aatataattt atataactct 720
gatgtttttg atgggaaggt tcagagggga ttaatcgtgt ttcatacttc tacagaacct 780
tcggttaatt acgatttatt tggtgctcaa ggacagtatt caaatacact attaagaata 840
tatagagata ataaaacgat taactctgaa aacatgcata ttgatatata tttatataca 900
agt 903

<210> 2
<211> 301
<212> PRT
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(301)
<223> fusion protein

<400> 2
Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
20 25 30
Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
35 40 45
Trp Trp Glu Leu Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
50 55 60
Gly Gly Gly Ser Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu
65 70 75 80
Arg Lys Lys Ser Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln
85 90 95
Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His
100 105 110
Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp
115 120 125
His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile
130 135 140
Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr
145 150 155 160
Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr
165 170 175
Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys
180 185 190
Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn Thr Val Pro Leu
195 200 205
Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val Gln Glu Leu Asp
210 215 220
Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser
225 230 235 240
Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Thr
245 250 255
Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln
260 265 270
Tyr Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn
275 280 285
Ser Glu Asn Met His Ile Asp Ile Tyr Leu Tyr Thr Ser
290 295 300

<210> 3
<211> 1107
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(1107)
<223> coding sequence of fusion protein

<400> 3
gcacccatgg cagaaggagg agggcagaat catcacgaag tggtgaagtt catggatgtc 60
tatcagcgca gctactgcca tccaatcgag accctggtgg acatcttcca ggagtaccct 120
gatgagatcg agtacatctt caagccatcc tgtgtgcccc tgatgcgatg cgggggctgc 180
tgcaatgacg agggcctgga gtgtgtgccc actgaggagt ccaacatcac catgcagatt 240
atgcggatca aacctcacca aggccagcac ataggagaga tgagcttcct acagcacaac 300
aaatgtgaat gcagaccaaa gaaagataga gcaagacaag aaaaatgtga caagccgagg 360
cggggtggag gcggttcagg cggaggtggc tctggcggtg gcggatcgag cgagaaaagc 420
gaagaaataa atgaaaaaga tttgcgaaaa aagtctgaat tgcagggaac agctttaggc 480

aatcttaaac aaatctatta ttacaatgaa aaagctaaaa ctgaaaataa agagagtcac 540
gatcaatttt tacagcatac tatattgttt aaaggctttt ttacagatca ttcgtggtat 600
aacgatttat tagtagattt tgattcaaag gatattgttg ataaatataa agggaaaaaa 660
gtagacttgt atggtgctta ttatggttat caatgtgcgg gtggtacacc aaacaaaaca 720
gcttgtatgt atggtggtgt aacgttacat gataataatc gattgaccga agagaaaaaa 780
gtgccgatca atttatggct agacggtaaa caaaatacag tacctttgga aacggttaaa 840
acgaataaga aaaatgtaac tgttcaggag ttggatcttc aagcaagacg ttatttacag 900
gaaaaatata atttatataa ctctgatgtt tttgatggga aggttcagag gggattaatc 960
gtgtttcata cttctacaga accttcggtt aattacgatt tatttggtgc tcaaggacag 1020
tattcaaata cactattaag aatatataga gataataaaa cgattaactc tgaaaacatg 1080
catattgata tatatttata tacaagt 1107

<210> 4
<211> 369
<212> PRT
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(369)
<223> fusion protein

<400> 4
Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys
1 5 10 15
Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu
20 25 30
Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys
35 40 45
Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
50 55 60
Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile
65 70 75 80
Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe
85 90 95
Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg
100 105 110
Gln Glu Lys Cys Asp Lys Pro Arg Arg Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Lys Ser Glu Glu Ile Asn
130 135 140
Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly Thr Ala Leu Gly
145 150 155 160
Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
165 170 175
Lys Glu Ser His Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly
180 185 190
Phe Phe Thr Asp His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp
195 200 205
Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr
210 215 220
Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr
225 230 235 240
Ala Cys Met Tyr Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr
245 250 255
Glu Glu Lys Lys Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
260 265 270
Thr Val Pro Leu Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val
275 280 285
Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn
290 295 300
Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile
305 310 315 320

Val Phe His Thr Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly
325 330 335
Ala Gln Gly Gln Tyr Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn
340 345 350
Lys Thr Ile Asn Ser Glu Asn Met His Ile Asp Ile Tyr Leu Tyr Thr
355 360 365
Ser

<210> 5
<211> 45
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(45)
<223> primer

<400> 5
ggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcg 45

<210> 6
<211> 15
<212> PRT
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(15)
<223> linker peptide

<400> 6

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 7
<211> 34
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(34)
<223> primer

<400> 7
gagcccgggc agcgagaaaa gcgaagaaat aaat 34

<210> 8
<211> 40
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(40)
<223> primer

<400> 8
gtgcggccgc acttgtatat aaatatatat caatatgcat 40

<210> 9
<211> 28
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(28)
<223> primer

<400> 9
gagcccgggc aattccgata gcgagtgt 28

<210> 10
<211> 28
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(28)
<223> primer

<400> 10
gtgcggccgc tctaagttcc caccattt 28

<210> 11
<211> 31
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(31)
<223> primer

<400> 11
gagcccgggc gcacccatgg cagaaggagg a 31

<210> 12
<211> 55
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(55)
<223> primer

<400> 12
gtgcggccgc ccgcctcggc ttgtcacatt tttcttgtct tgctctatct ttctt 55

<210> 13
<211> 54
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(54)
<223> primer

<400> 13

gccagagcca cctccgcctg aaccgcctcc acctctaagt tcccaccatt tcag 54

<210> 14
<211> 60
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(60)
<223> primer

<400> 14
tcaggcggag gtggctctgg cggtggcgga tcgagcgaga aaagcgaaga ataaatgaa 60

<210> 15
<211> 57
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (1)..(57)
<223> primer

<400> 15
gccagagcca cctccgcctg aaccgcctcc accccgcctc ggcttgtcac atttttc 57